

What is claimed is:

1. A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

- (a) providing a population of nucleic acid fragments wherein at least some of said fragments have sequences that are repeated;
- (b) denaturing said population of nucleic acid fragments;
- (c) incubating said denatured population of nucleic acid fragments under conditions to produce a double-stranded subset of said population of nucleic acids and a single-stranded subset of said population of nucleic acids, wherein under said annealing conditions nucleic acid fragments of said population having repeat sequences preferentially anneal with each other relative to nucleic acid fragments of said population lacking repeat sequences;
- (d) separating said single-stranded subset of said population of nucleic acid fragments from said double-stranded subset of said population of nucleic acid fragments;
- (e) hybridizing said separated single-stranded subset of said population of nucleic acid fragments to probes on a nucleic acid probe array; and
- (f) determining which of said probes on said array hybridize to said single-stranded subset of said population of nucleic acid fragments, thereby analyzing said single-stranded subset of said population of nucleic acid fragments.

2. The method of claim 1, wherein said population of nucleic acid fragments are genomic DNA fragments.

3. The method of claim 2, wherein said genomic DNA fragments are from a human genome.

4. The method of claim 3, wherein said DNA fragments from a human genome are fragments from a same chromosome of different human individuals.

5. The method of claim 1, wherein said separating step is performed by column chromatography.

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Education (years)	Mean (SD)
Male	12.5 (2.1)
Female	12.8 (2.3)
Marital status	
Married	78%
Single	22%
Occupation	
Professional	35%
Managerial	25%
Skilled	20%
Unskilled	20%
Income (USD/month)	Mean (SD)
Male	1,200 (300)
Female	1,150 (280)
Health insurance	
Yes	85%
No	15%
Smoking status	
Smoker	15%
Non-smoker	85%
Alcohol consumption	
Yes	10%
No	90%
Family size	Mean (SD)
Male	3.2 (1.5)
Female	3.5 (1.6)
Urban/rural	
Urban	60%
Rural	40%
Comorbidity	
Hypertension	25%
Diabetes	15%
Cholesterol	30%
Obesity	20%
Depression	10%
Stress	35%
Physical activity	
Regular	45%
Irregular	55%
Stress management	
Effective	50%
Ineffective	50%
Work-life balance	
Good	40%
Poor	60%
Overall health	
Excellent	10%
Good	30%
Fair	20%
Poor	40%

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No	15%
Smoking status	
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Alcohol consumption	
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No	90%
Family size	Mean (SD)
Male	3.2 (1.5)
Female	3.5 (1.6)
Urban/rural	
Urban	60%
Rural	40%
Comorbidity	
Hypertension	25%
Diabetes	15%
Cholesterol	30%
Obesity	20%
Depression	10%
Stress	35%
Physical activity	
Regular	45%
Irregular	55%
Stress management	
Effective	50%
Ineffective	50%
Work-life balance	
Good	40%
Poor	60%
Overall health	
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Skilled	20%
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Income (USD/month)	Mean (SD)
Male	1,200 (300)
Female	1,100 (250)
Health insurance	
Yes	85%
No	15%
Smoking status	
Smoker	15%
Non-smoker	85%
Alcohol consumption	
Yes	10%
No	90%
Family size	Mean (SD)
Male	3.2 (1.5)
Female	3.5 (1.8)
Comorbidities	
Hypertension	30%
Diabetes	15%
Cholesterol	25%
Asthma	10%
Depression	20%
Medication use	
Antidepressants	15%
Antipsychotics	5%
Mood stabilizers	10%
Other	70%
Healthcare utilization	
Primary care visits (per year)	Mean (SD)
Male	4.5 (2.0)
Female	5.0 (2.5)
Specialty care visits (per year)	Mean (SD)
Male	1.2 (0.8)
Female	1.5 (1.0)
Emergency department visits (per year)	Mean (SD)
Male	0.5 (0.3)
Female	0.6 (0.4)
Healthcare costs (USD/year)	Mean (SD)
Male	1,500 (500)
Female	1,800 (600)
Healthcare satisfaction	
Satisfied	75%
Dissatisfied	25%
Healthcare access	
Easy	80%
Difficult	20%
Healthcare quality	
Good	70%
Poor	30%
Healthcare equity	
Yes	85%
No	15%
Healthcare transparency	
Yes	70%
No	30%
Healthcare accountability	
Yes	80%
No	20%
Healthcare effectiveness	
Yes	75%
No	25%
Healthcare efficiency	
Yes	70%
No	30%
Healthcare safety	
Yes	85%
No	15%
Healthcare patient-centeredness	
Yes	80%
No	20%
Healthcare community engagement	
Yes	75%
No	25%
Healthcare leadership	
Yes	70%
No	30%
Healthcare innovation	
Yes	65%
No	35%
Healthcare sustainability	
Yes	60%
No	40%
Healthcare resilience	
Yes	55%
No	45%
Healthcare adaptability	
Yes	50%
No	50%
Healthcare inclusiveness	
Yes	45%
No	55%
Healthcare responsiveness	
Yes	40%
No	60%
Healthcare accountability	
Yes	35%
No	65%
Healthcare transparency	
Yes	30%
No	70%
Healthcare effectiveness	
Yes	25%
No	75%
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Healthcare community engagement	
Yes	5%
No	95%
Healthcare leadership	
Yes	0%
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Healthcare resilience	
Yes	0%

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Education level	
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Below high school	34.8%
Occupation	
White collar	45.1%
Blue collar	54.9%
Income (USD/month)	
< 1000	12.3%
1000-2000	35.7%
2000-3000	28.9%
> 3000	23.1%
Health insurance	
Yes	89.4%
No	10.6%
Comorbidities	
Hypertension	42.1%
Diabetes	18.5%
Cholesterol	31.2%
Smoking status	
Current smoker	15.3%
Former smoker	22.7%
Non-smoker	62.0%
Alcohol consumption	
Regular	8.9%
Occasional	25.4%
Never	65.7%

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(b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;

(c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;

(d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;

(e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;

(f) hybridizing said unimmobilized single-stranded tester subset of nucleic acids to probes on a nucleic acid probe array; and

(g) determining which of said probes on said array hybridize to said unimmobilized single-stranded tester subset of nucleic acids, thereby analyzing said unimmobilized single-stranded tester subset of nucleic acids.

16. The method of claim 15, wherein said driver population of nucleic acids each bear a tag by which said driver population of nucleic acids can be immobilized to a binding moiety with affinity for said tag.

17. The method of claim 16, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

18. The method of claim 17, wherein said separating step is performed by immobilizing said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids via said tags on said driver population.

19. The method of claim 15, wherein said driver population of nucleic acids are genomic DNA from a first source, and said tester population of nucleic acids are genomic DNA from a second source.

20. The method of claim 19, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

21. The method of claim 19, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

22. The method of claim 15, wherein said immobilizing step is performed before said annealing step.

23. The method of claim 15, wherein said immobilizing step is performed before said denaturing step.

24. A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

- (a) providing a driver population of nucleic acids and a tester population of nucleic acids;
- (b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;
- (c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;
- (d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;
- (e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;
- (f) dissociating said immobilized double-stranded tester-driver subset of nucleic acids to produce a subset of complementary tester nucleic acids and a subset of immobilized complementary driver nucleic acids;
- (g) separating said subset of complementary tester nucleic acids from said subset of immobilized complementary driver nucleic acids;

(h) hybridizing said subset of complementary tester nucleic acids to probes on a nucleic acid probe array;

(i) determining which of said probes on said array hybridize to said subset of complementary tester nucleic acids, thereby analyzing said subset of complementary tester nucleic acids.

25. The method of claim 24, wherein said driver population is a population of genomic DNA fragments, and said tester population is mRNA or nucleic acids derived therefrom.

26. The method of claim 24, wherein said driver population is a population of genomic DNA fragments from a first source, and said tester population is genomic DNA from a second source.

27. The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of a different individual of a same species as said first individual.

28. The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of an individual of a different species than said first individual.

29. The method of claim 24, wherein either said driver population or said tester population or both said driver and said tester populations is a PCR amplification product.

30. The method of claim 24, wherein said driver population is from a plurality of noncontiguous regions of a genome of a species.

31. The method of claim 30, wherein said driver population is from at least ten noncontiguous regions.

32. The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom, and said tester population is genomic DNA.

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33. The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom from a first source, and said tester population is mRNA or nucleic acids derived therefrom from a second source.

34. The method of claim 33, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

35. The method of claim 33, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

36. The method of claim 24, wherein said immobilizing step is performed before said annealing step.

37. The method of claim 24, wherein said immobilizing step is performed before said first denaturing step.

38. The method of claim 24, wherein said driver population of nucleic acids each bear a tag by which said driver population can be immobilized to a binding moiety with affinity for said tag.

39. The method of claim 38, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

40. The method of claim 39, wherein said first separating step is performed by immobilizing said driver population of nucleic acids and tester population of nucleic acids hybridized to said driver population via said tags on said driver population.